

-continued

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**1.-38. (canceled)**

**39.** A method for reducing an error rate in sequence reads of a double-stranded target nucleic acid molecule, comprising:

- a) ligating the double-stranded target nucleic acid molecule to a double-stranded cypher to form a cypher-target nucleic acid complex, wherein the double-stranded cypher comprises a random or partially random identifier sequence that alone or in combination with an end of the target nucleic acid molecule uniquely labels the double-stranded target nucleic acid molecule;
- b) amplifying each strand of the cypher-target nucleic acid complex to produce a plurality of cypher-target ampli-

fication products from each of a first strand and a complementary second strand of the cypher-target nucleic acid complex;

- (c) sequencing the cypher-target amplification products to produce a plurality of first-strand sequencing reads and a plurality of second-strand sequencing reads; and
- (d) comparing the first-strand sequencing reads with the second-strand sequencing reads, and generating an error-corrected sequence of the double-stranded target nucleic acid molecule by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand.